

IN THE SEQUENCE LISTING

Kindly enter the attached Sequence Listing in lieu of the original translation.

10/534002

SEQUENCE LISTING JC20 Rec'd PCT/PTO 05 MAY 2005

<110> NARIMATSU, Hisashi
SATO, Takashi
GOTOH, Masanori

<120> METHOD OF DETECTING BONE PAGET'S DISEASE

<130> 159-88 / YCT-882

<140> US

<141> 2005-05-05

<150> PCT/JP2003/014211

<151> 2003-11-07

<150> JP2002-323438

<151> 2002-11-07

<160> 70

<170> MS Word

<210> 1

<211> 2649

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (2649)

<400> 1
atg gct gtg cgc tct cgc cgc ccg tgg atg agc gtg gca tta ggg ctg 48
Met Ala Val Arg Ser Arg Arg Pro Trp Met Ser Val Ala Leu Gly Leu
1 5 10 15

gtg ctg ggc ttc acc gcc gcg tcc tgg ctc atc gcc ccc agg gtg gcg 96
 Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala
 20 25 30

gag ctg agc gag agg aag aga cgt ggc tcc agc ctc tgc tcc tac tac 144
 Glu Leu Ser Glu Arg Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr .
 35 40 45

ggc cgc tct gct gct ggc ccc cgc gcc ggc gct cag cag ccg ctc ccc
 Gly Arg Ser Ala Ala Gly Pro Arg Ala Gly Ala Gln Gln Pro Leu Pro
 50 55 60

cag ccc cag tcc cga cca cg^g cag gag cag tcg cc^g ccc ccc gc^g cgc
 Gln Pro Gln Ser Arg Pro Arg Gln Glu Gln Ser Pro Pro Pro Ala Arg
 65 70 75 80

```

cag gat ctc cag ggg cca ccg ctg ccc gag gca gca ccc ggg atc acc      288
Gln Asp Leu Gln Gly Pro Pro Leu Pro Glu Ala Ala Pro Gly Ile Thr
   85           90           95

```

agt ttt cga agc agc ccc tgg cag cag cca cct ccg ctg cag cag cgg	336
Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Pro Pro Leu Gln Gln Arg	
100 105 110	
cg g cga gga cgc gag cct gag ggc gcg acg ggg ctt ccc ggt gct cca	384
Arg Arg Gly Arg Glu Pro Glu Gly Ala Thr Gly Leu Pro Gly Ala Pro	
115 120 125	
g c g gcc gag ggg gag ccc gag gag gac ggg ggc g c g gct ggg cag	432
Ala Ala Glu Gly Glu Pro Glu Glu Asp Gly Gly Ala Ala Gly Gln	
130 135 140	
cg g aga gac ggc cg g gg g agt agc cac aac ggc agc gg g gac gg g	480
Arg Arg Asp Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly	
145 150 155 160	
g g c gct g c c g c c cc g agc g c c ccc cg g gac ttc ctg tac gt g g g g	528
Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly	
165 170 175	
gt g atg acc g c g cag aag tac ctg g c g agc cgc g c g ctg g c c g c g cag	576
Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln	
180 185 190	
cg g acc tgg g c g cgt ttc atc cc g g c g cgc gt g g g ttc ttt tcc ag c	624
Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser	
195 200 205	
c a g c a g ccc ccc aac g c c g c g c a g ccc c g c c c a g c g c c c t g t c a tc	672
Gln Gln Pro Pro Asn Ala Gly Gln Pro Pro Pro Pro Leu Pro Val Ile	
210 215 220	
g c g cta cc g ggt gt g gac gac tcc tat cct ccc c a g aaa aag tcc ttc	720
Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe	
225 230 235 240	
at g at g atc aag tac at g cac gac cac tac ctg gac aag tat gag tgg	768
Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu Trp	
245 250 255	
t t c at g cgc g c c gac gac gat g t c tac atc aaa ggt gat aaa t t a gaa	816
Phe Met Arg Ala Asp Asp Val Tyr Ile Lys Gly Asp Lys Leu Glu	
260 265 270	
gag ttt ctt aga tcg cta aac agc agt aag cct ctc tac ctg gga cag	864
Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu Gly Gln	
275 280 285	
act ggc ctg ggg aat att gaa gag ctt gga aag ctg gga ctg gag cct	912
Thr Gly Leu Gly Asn Ile Glu Glu Leu Gly Lys Leu Gly Leu Glu Pro	
290 295 300	
gg g gaa aac ttc tgt at g gga gga cct g g c at g atc ttt agc c g a gaa	960
Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser Arg Glu	
305 310 315 320	

gtt ctc agg agg atg gtg cca cat att ggt gaa tgc ctt aga gaa atg Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg Glu Met	325	330	335	1008
tac acg act cat gag gat gtg gaa gta gga aga tgc gtt cgc cgt ttt Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg Arg Phe	340	345	350	1056
ggg ggg act cag tgt gtc tgg tct tac gag atg caa caa ctg ttc cat Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu Phe His	355	360	365	1104
gaa aat tat gaa cac aat cgg aag ggt tac atc caa gac ctt cac aat Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu His Asn	370	375	380	1152
agc aaa atc cat gca gcc ata aca ctt cat ccc aac aaa agg cct gca Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg Pro Ala	385	390	395	1200
tac caa tac agg ctg cat aat tac atg ctc agc cgc aaa att tct gaa Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile Ser Glu	405	410	415	1248
ctt cgc tac cgc acc atc cag ctc cac agg gaa agt gcc ctg atg agc Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu Met Ser	420	425	430	1296
aag ctc agt aac aca gaa gtg agc aaa gag gac cag cag ctg gga gtg Lys Leu Ser Asn Thr Glu Val Ser Lys Glu Asp Gln Gln Leu Gly Val	435	440	445	1344
ata cct tct ttc aac cac ttc cag cct cgg gag aga aat gaa gtg ata Ile Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu Val Ile	450	455	460	1392
gaa tgg gag ttc ctg aca ggg aag ctt cta tac tca gca gct gag aac Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala Glu Asn	465	470	475	1440
cag ccc cct cga cag agc ctc agt agc att tta aga aca gca ctg gat Gln Pro Pro Arg Gln Ser Leu Ser Ser Ile Leu Arg Thr Ala Leu Asp	485	490	495	1488
gat acc gtc cta cag gtg atg gag atg atc aat gag aat gcc aag agc Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala Lys Ser	500	505	510	1536
aga gga cgg ctc att gac ttc aag gaa att cag tat ggc tac cgc aga Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr Arg Arg	515	520	525	1584
gtt aac ccc atg cac ggg gtg gag tac att ttg gat tta ctc ctt tta Val Asn Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu Leu	530	535	540	1632

tac aaa aga cac aag gga agg aaa ctg act gtg cca gtg aga cgt cat Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg Arg His 545 550 555 560	1680
gcc tat ctt cag cag ttg ttc agc aag cct ttc ttc aga gag acc gaa Ala Tyr Leu Gln Gln Leu Phe Ser Lys Pro Phe Phe Arg Glu Thr Glu 565 570 575	1728
gag cta gat gtc aac agt ctt gtg gag agt att aac agt gaa act cag Glu Leu Asp Val Asn Ser Leu Val Glu Ser Ile Asn Ser Glu Thr Gln 580 585 590	1776
tca ttc tcc ttt ata tct aat tct tta aag ata tta tct tct ttt caa Ser Phe Ser Phe Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser Phe Gln 595 600 605	1824
ggg gcc aaa gaa atg gga ggg cac aat gaa aag aaa gta cac att ctc Gly Ala Lys Glu Met Gly His Asn Glu Lys Lys Val His Ile Leu 610 615 620	1872
gtt cct ctc atc gga agg tat gac att ttc ttg aga ttc atg gag aac Val Pro Leu Ile Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met Glu Asn 625 630 635 640	1920
ttt gaa aac atg tgt ctt atc cca aag cag aat gta aag ttg gtc att Phe Glu Asn Met Cys Leu Ile Pro Lys Gln Asn Val Lys Leu Val Ile 645 650 655	1968
atc ctt ttc agt agg gat tct ggc caa gac tcc agc aag cat att gag Ile Leu Phe Ser Arg Asp Ser Gly Gln Asp Ser Ser Lys His Ile Glu 660 665 670	2016
ctg ata aaa ggg tac cag aac aag tac ccc aaa gca gaa atg acc ctg Leu Ile Lys Gly Tyr Gln Asn Lys Tyr Pro Lys Ala Glu Met Thr Leu 675 680 685	2064
atc cca atg aag gga gag ttt tcc aga ggt ctt ggt ctt gaa atg gct Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Glu Met Ala 690 695 700	2112
tct gcc cag ttt gac aat gac act ttg ctg cta ttt tgt gat gtt gac Ser Ala Gln Phe Asp Asn Asp Thr Leu Leu Phe Cys Asp Val Asp 705 710 715 720	2160
ttg atc ttc aga gaa gat ttt ctc caa cga tgt aga gac aat aca att Leu Ile Phe Arg Glu Asp Phe Leu Gln Arg Cys Arg Asp Asn Thr Ile 725 730 735	2208
cag gga caa cag gtg tac tat ccc atc atc ttt agc cag tat gac cca Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr Asp Pro 740 745 750	2256
aag gta aca aac ggg gga aat cct ccc act gat ggt tac ttc ata ttc Lys Val Thr Asn Gly Gly Asn Pro Pro Thr Asp Gly Tyr Phe Ile Phe 755 760 765	2304

tca aaa aag act gga ttt tgg aga gac tat gga tat ggc atc acc tgt Ser Lys Lys Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile Thr Cys 770 775 780	2352
att tac aaa agt gat ctt cta ggt gca ggt gga ttt gat acc tca ata Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr Ser Ile 785 790 795 800	2400
caa ggc tgg gga cta gaa gat gta gat ctc tac aat aaa gtc att cta Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val Ile Leu 805 810 815	2448
tct ggc tta agg cca ttc aga agc caa gaa gta gga gtg gtg cat att Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val His Ile 820 825 830	2496
ttc cat cca gtt cat tgt gat cct aac ttg gac cct aag cag tat aag Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys 835 840 845	2544
atg tgc tta gga tcc aag gca agt act ttc gcc tca acc atg caa ctg Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met Gln Leu 850 855 860	2592
gct gaa ctc tgg ctt gaa aaa cat tta ggt gtc agg tac aat cga act Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Tyr Asn Arg Thr 865 870 875 880	2640
ctc tcc tga Leu Ser	2649

<210> 2			
<211> 882			
<212> PRT			
<213> Homo sapiens			
<400> 2			
Met Ala Val Arg Ser Arg Arg Pro Trp Met Ser Val Ala Leu Gly Leu 1 5 10 15			
Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala 20 25 30			
Glu Leu Ser Glu Arg Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr 35 40 45			
Gly Arg Ser Ala Ala Gly Pro Arg Ala Gly Ala Gln Gln Pro Leu Pro 50 55 60			
Gln Pro Gln Ser Arg Pro Arg Gln Glu Gln Ser Pro Pro Pro Ala Arg 65 70 75 80			
Gln Asp Leu Gln Gly Pro Pro Leu Pro Glu Ala Ala Pro Gly Ile Thr 85 90 95			

Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Pro Pro Leu Gln Gln Arg
100 105 110

Arg Arg Gly Arg Glu Pro Glu Gly Ala Thr Gly Leu Pro Gly Ala Pro
115 120 125

Ala Ala Glu Gly Glu Pro Glu Glu Asp Gly Gly Ala Ala Gly Gln
130 135 140

Arg Arg Asp Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
145 150 155 160

Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly
165 170 175

Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
180 185 190

Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
195 200 205

Gln Gln Pro Pro Asn Ala Gly Gln Pro Pro Pro Pro Leu Pro Val Ile
210 215 220

Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
225 230 235 240

Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu Trp
245 250 255

Phe Met Arg Ala Asp Asp Val Tyr Ile Lys Gly Asp Lys Leu Glu
260 265 270

Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu Gly Gln
275 280 285

Thr Gly Leu Gly Asn Ile Glu Glu Leu Gly Lys Leu Gly Leu Glu Pro
290 295 300

Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser Arg Glu
305 310 315 320

Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg Glu Met
325 330 335

Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg Arg Phe
340 345 350

Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu Phe His
355 360 365

Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu His Asn
370 375 380

Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg Pro Ala
385 390 395 400

Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile Ser Glu
405 410 415

Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu Met Ser
420 425 430

Lys Leu Ser Asn Thr Glu Val Ser Lys Glu Asp Gln Gln Leu Gly Val
435 440 445

Ile Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu Val Ile
450 455 460

Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala Glu Asn
465 470 475 480

Gln Pro Pro Arg Gln Ser Leu Ser Ser Ile Leu Arg Thr Ala Leu Asp
485 490 495

Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala Lys Ser
500 505 510

Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr Arg Arg
515 520 525

Val Asn Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu Leu Leu
530 535 540

Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg Arg His
545 550 555 560

Ala Tyr Leu Gln Gln Leu Phe Ser Lys Pro Phe Phe Arg Glu Thr Glu
565 570 575

Glu Leu Asp Val Asn Ser Leu Val Glu Ser Ile Asn Ser Glu Thr Gln
580 585 590

Ser Phe Ser Phe Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser Phe Gln
595 600 605

Gly Ala Lys Glu Met Gly His Asn Glu Lys Lys Val His Ile Leu
610 615 620

Val Pro Leu Ile Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met Glu Asn
625 630 635 640

Phe Glu Asn Met Cys Leu Ile Pro Lys Gln Asn Val Lys Leu Val Ile
645 650 655

Ile Leu Phe Ser Arg Asp Ser Gly Gln Asp Ser Ser Lys His Ile Glu
660 665 670

Leu Ile Lys Gly Tyr Gln Asn Lys Tyr Pro Lys Ala Glu Met Thr Leu
675 680 685

Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu Met Ala
690 695 700

Ser Ala Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp Val Asp
705 710 715 720

Leu Ile Phe Arg Glu Asp Phe Leu Gln Arg Cys Arg Asp Asn Thr Ile
725 730 735

Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr Asp Pro
740 745 750

Lys Val Thr Asn Gly Gly Asn Pro Pro Thr Asp Gly Tyr Phe Ile Phe
755 760 765

Ser Lys Lys Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile Thr Cys
770 775 780

Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr Ser Ile
785 790 795 800

Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val Ile Leu
805 810 815

Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val His Ile
820 825 830

Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys
835 840 845

Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met Gln Leu
850 855 860

Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Tyr Asn Arg Thr
865 870 875 880

Leu Ser

<210> 3
<211> 2328
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2328)

<400> 3
atg cgg gca tcg ctg ctg tcg gtg ctg cgg ccc gca ggg ccc gtg
Met Arg Ala Ser Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val
1 5 10 15

gcc gtg ggc atc tcc ctg ggc ttc acc ctg agc ctc agc gtc acc
Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr
20 25 30

48

96

tgg	gtg	gag	gag	ccg	tgc	ggc	cca	ggc	ccg	ccc	caa	cct	gga	gac	tct	144
Trp	Val	Glu	Glu	Pro	Cys	Gly	Pro	Gly	Pro	Pro	Gln	Pro	Gly	Asp	Ser	
35							40					45				
gag	ctg	ccg	ccg	cgc	ggc	aac	acc	aac	gcg	gcg	cgc	ccg	ccc	aac	tcg	192
Glu	Leu	Pro	Pro	Arg	Gly	Asn	Thr	Asn	Ala	Ala	Arg	Arg	Arg	Pro	Asn	Ser
50							55				60					
gtg	cag	ccc	gga	gcg	gag	cgc	gag	aag	ccc	ggg	gcc	ggc	gaa	ggc	gcc	240
Val	Gln	Pro	Gly	Ala	Glu	Arg	Glu	Lys	Pro	Gly	Ala	Gly	Glu	Gly	Ala	
65							70			75		80				
ggg	gag	aat	tgg	gag	ccg	cgc	gtc	ttg	ccc	tac	cac	cct	gca	cag	ccc	288
Gly	Glu	Asn	Trp	Glu	Pro	Arg	Val	Leu	Pro	Tyr	His	Pro	Ala	Gln	Pro	
85							90			95						
ggc	cag	gcc	gcc	aaa	aag	gcc	gtc	agg	acc	cgc	tac	atc	agc	acg	gag	336
Gly	Gln	Ala	Ala	Lys	Lys	Ala	Val	Arg	Thr	Arg	Tyr	Ile	Ser	Thr	Glu	
100							105			110						
ctg	ggc	atc	agg	cag	agg	ctg	ctg	gtg	gcg	gtg	ctg	acc	tct	cag	acc	384
Leu	Gly	Ile	Arg	Gln	Arg	Leu	Leu	Val	Ala	Val	Leu	Thr	Ser	Gln	Thr	
115							120			125						
acg	ctg	ccc	acg	ctg	ggc	gtg	gcc	gtg	aac	cgc	acg	ctg	ggg	cac	cgg	432
Thr	Leu	Pro	Thr	Leu	Gly	Val	Ala	Val	Asn	Arg	Thr	Leu	Gly	His	Arg	
130							135			140						
ctg	gag	cgt	gtg	gtg	ttc	ctg	acg	ggc	gca	cg	ggc	cgc	cg	gg	cc	480
Leu	Glu	Arg	Val	Val	Phe	Leu	Thr	Gly	Ala	Arg	Gly	Arg	Arg	Ala	Pro	
145							150			155		160				
cct	ggc	atg	gca	gtg	gtg	acg	ctg	ggc	gag	gag	cga	ccc	att	gga	cac	528
Pro	Gly	Met	Ala	Val	Val	Thr	Leu	Gly	Glu	Glu	Arg	Pro	Ile	Gly	His	
165							170			175						
ctg	cac	ctg	g	ctg	cgc	cac	ctg	ctg	gag	cag	cac	ggc	gac	gac	ttt	576
Leu	His	Leu	Ala	Leu	Arg	His	Leu	Leu	Glu	Gln	His	Gly	Asp	Asp	Phe	
180							185			190						
gac	tgg	t	tc	tc	gt	c	c	t	g	ac	ac	ac	tg	ac	gg	624
Asp	Trp	Phe	Phe	Leu	Val	Pro	Asp	Thr	Th	Y	Th	Glu	Ala	His	Gly	
195							200			205						
ctg	gca	cgc	cta	act	ggc	cac	ctc	agc	ctg	ggc	tcc	ggc	ggc	cac	ctg	672
Leu	Ala	Arg	Leu	Thr	Gly	His	Leu	Ser	Leu	Ala	Ser	Ala	Ala	His	Leu	
210							215			220						
tac	ctg	ggc	ccg	ccc	cag	gac	t	tc	atc	ggc	gga	gag	ccc	acc	ccc	720
Tyr	Leu	Gly	Arg	Pro	Gln	Asp	Phe	Ile	Gly	Gly	Glu	Pro	Thr	Pro	Gly	
225							230			235		240				
cgc	tac	tgc	cac	gga	ggc	ttt	ggg	gt	ct	tg	tc	cg	at	ct	ct	768
Arg	Tyr	Cys	His	Gly	Gly	Phe	Gly	Val	Leu	Leu	Ser	Arg	Met	Leu	Leu	
245							250			255						

caa caa ctg cgc ccc cac ctg gaa ggc tgc cgc aac gac atc gtc agt Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile Val Ser 260 265 270	816
gcg cgc cct gac gag tgg ctg ggt cgc tgc att ctc gat gcc acc ggg Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly 275 280 285	864
gtg ggc tgc act ggt gac cac gag ggg gtg cac tat agc cat ctg gag Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr Ser His Leu Glu 290 295 300	912
ctg agc cct ggg gag cca gtg cag gag ggg gac cct cat ttc cga agt Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro His Phe Arg Ser 305 310 315 320	960
gcc ctg aca gcc cac cct gtg cgt gac cct gtg cac atg tac cag ctg Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu 325 330 335	1008
cac aaa gct ttc gcc cga gct gaa ctg gaa cgc acg tac cag gag atc His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg Thr Tyr Gln Glu Ile 340 345 350	1056
cag gag tta cag tgg gag atc cag aat acc agc cat ctg gcc gtt gat Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser His Leu Ala Val Asp 355 360 365	1104
ggg gac cgg gca gct gct tgg ccc gtg ggt att cca gca cca tcc cgc Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg 370 375 380	1152
ccg gcc tcc cgc ttt gag gtg ctg cgc tgg gac tac ttc acg gag cag Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln 385 390 395 400	1200
cac gct ttc tcc tgc gcc gat ggc tca ccc cgc tgc cca ctg cgt ggg His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly 405 410 415	1248
gct gac cgg gct gat gtg gcc gat gtt ctg ggg aca gct cta gag gag Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu 420 425 430	1296
ctg aac cgc cgc tac cac ccg gcc ttg cgg ctc cag aag cag cag ctg Leu Asn Arg Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu 435 440 445	1344
gtg aat ggc tac cga cgc ttt gat ccg gcc cgg ggt atg gaa tac acg Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr 450 455 460	1392
ctg gac ttg cag ctg gag gca ctg acc ccc cag gga ggc cgc cgg ccc Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro 465 470 475 480	1440

ctc act cgc cga gtg cag ctg ctc cgg ccg ctg agc cgc gtg gag atc Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile 485 490 495	1488
ttg cct gtg ccc tat gtc act gag gcc tca cgt ctc act gtg ctg ctg Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu 500 505 510	1536
cct cta gct gcg gct gag cgt gac ctg gcc cct ggc ttc ttg gag gcc Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe Leu Glu Ala 515 520 525	1584
ttt gcc act gca gca ctg gag cct ggt gat gct gcg gca gcc ctg acc Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr 530 535 540	1632
ctg ctg cta ctg tat gag ccg cgc cag gcc cag cgc gtg gcc cat gca Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Val Ala His Ala 545 550 555 560	1680
gat gtc ttc gca cct gtc aag gcc cac gtg gca gag ctg gag cggt cgt Asp Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg 565 570 575	1728
tcc ccc ggt gcc cgg gtg cca tgg ctc agt gtg cag aca gcc gca ccc Phe Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro 580 585 590	1776
tca cca ctg cgc ctc atg gat cta ctc tcc aag aag cac ccg ctg gac Ser Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp 595 600 605	1824
aca ctg ttc ctg ctg gcc ggg cca gac acg gtg ctc acg cct gac ttc Thr Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe 610 615 620	1872
ctg aac cgc tgc cgc atg cat gcc atc tcc ggc tgg cag gcc ttc ttt Leu Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe 625 630 635 640	1920
ccc atg cat ttc caa gcc ttc cac cca gct gtg gcc cca cca caa ggg Pro Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly 645 650 655	1968
cct ggg ccc cca gag ctg ggc cgt gac act ggc cgc ttt gat cgc cag Pro Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln 660 665 670	2016
gca gcc agc gag gcc tgc ttc tac aac tcc gac tac gtg gca gcc cgt Ala Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg 675 680 685	2064
ggg cgc ctg gcg gca gcc tca gaa caa gaa gag gag ctg ctg gag agc Gly Arg Leu Ala Ala Ser Glu Gln Glu Glu Leu Leu Glu Ser 690 695 700	2112

ctg gat gtg tac gag ctg ttc ctc cac ttc tcc agt ctg cat gtg ctg 2160
Leu Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
705 710 715 720

cgg gcg gtg gag ccg gcg ctg ctg cag cgc tac cgg gcc cag acg tgc 2208
Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr Cys
725 730 735

agc gcg agg ctc agt gag gac ctg tac cac cgc tgc ctc cag agc gtg 2256
Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln Ser Val
740 745 750

ctt gag ggc ctc ggc tcc cga acc cag ctg gcc atg cta ctc ttt gaa 2304
Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu
755 760 765

cag gag cag ggc aac agc acc tga 2328
Gln Glu Gln Gly Asn Ser Thr
770 775

<210> 4
<211> 775
<212> PRT
<213> Homo sapiens

<400> 4
Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val
1 5 10 15

Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr
20 25 30

Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser
35 40 45

Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser
50 55 60

Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly Ala Gly Glu Gly Ala
65 70 75 80

Gly Glu Asn Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro
85 90 95

Gly Gln Ala Ala Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu
100 105 110

Leu Gly Ile Arg Gln Arg Leu Leu Val Ala Val Leu Thr Ser Gln Thr
115 120 125

Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg
130 135 140

Leu Glu Arg Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro
145 150 155 160

Pro Gly Met Ala Val Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His
165 170 175

Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe
180 185 190

Asp Trp Phe Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly
195 200 205

Leu Ala Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu
210 215 220

Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly
225 230 235 240

Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu Leu
245 250 255

Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile Val Ser
260 265 270

Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly
275 280 285

Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr Ser His Leu Glu
290 295 300

Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro His Phe Arg Ser
305 310 315 320

Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
325 330 335

His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg Thr Tyr Tyr Gln Glu Ile
340 345 350

Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser His Leu Ala Val Asp
355 360 365

Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
370 375 380

Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
385 390 395 400

His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
405 410 415

Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
420 425 430

Leu Asn Arg Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu
435 440 445

Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
450 455 460

Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro
 465 470 475 480
 Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
 485 490 495
 Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
 500 505 510
 Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe Leu Glu Ala
 515 520 525
 Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr
 530 535 540
 Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Val Ala His Ala
 545 550 555 560
 Asp Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg
 565 570 575
 Phe Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro
 580 585 590
 Ser Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp
 595 600 605
 Thr Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe
 610 615 620
 Leu Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe
 625 630 635 640
 Pro Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly
 645 650 655
 Pro Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln
 660 665 670
 Ala Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg
 675 680 685
 Gly Arg Leu Ala Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser
 690 695 700
 Leu Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
 705 710 715 720
 Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr Cys
 725 730 735
 Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln Ser Val
 740 745 750
 Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu
 755 760 765

Gln Glu Gln Gly Asn Ser Thr
770 775

```
<210> 5
<211> 1669
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> (41)..(1024)

<400>	5		55			
ctgcgagcgc	ctgccccatg	cggccggcc	tctccgcacg	atg ttc ccc tcg cgg	Met Phe Pro Ser Arg	
				1		5
agg aaa gca	gca gca ctg	ccc tgg gag	gac ggc agg	tcc ggg ttg ctc		103
Arg Lys Ala	Ala Gln Leu	Pro Trp Glu	Asp Gly Arg	Ser Gly Leu	Leu	
	10		15		20	
tcc ggc ggc	ctc cct cgg	aag tgt tcc	gtc ttc cac	ctg ttc gtg gcc		151
Ser Gly Gly	Leu Pro Arg	Lys Cys Ser	Val Phe His	Leu Phe Val	Ala	
	25		30		35	
tgc ctc tcg	ctg ggc ttc	tcc cta ctc	tgg ctg cag	ctc agc tgc		199
Cys Leu Ser	Leu Gly Phe	Phe Ser Leu	Leu Trp Leu	Gln Leu Ser	Cys	
	40		45		50	
tct ggg gac	gtg gcc cgg	gca gtc agg	gga caa ggg	cag gag acc tcg		247
Ser Gly Asp	Val Ala Arg	Ala Val Arg	Gly Gln Gly	Gln Glu Thr	Ser	
	55		60		65	
ggc cct ccc	cgc gcc tgc	ccc cca gag	ccg ccc cct	gag cac tgg gaa		295
Gly Pro Pro	Arg Ala Cys	Pro Pro Glu	Pro Pro Pro	Glu His Trp	Glu	
	70		75		80	
gaa gac gca	tcc tgg ggc	ccc cac cgc	ctg gca gtg	ctg gtg ccc ttc		343
Glu Asp Ala	Ser Trp Gly	Pro His Arg	Leu Ala Val	Leu Val Pro	Phe	
	90		95		100	
cgc gaa cgc	ttc gag gag	ctc ctg gtc	ttc gtg ccc	cac atg cgc cgc		391
Arg Glu Arg	Phe Glu Glu	Leu Leu Val	Phe Val Pro	His Met Arg	Arg	
	105		110		115	
ttc ctg agc	agg aag aag	atc cgg cac	cac atc tac	gtg ctc aac cag		439
Phe Leu Ser	Arg Lys Lys	Ile Arg His	His Ile Tyr	Val Leu Asn	Gln	
	120		125		130	
gtg gac cac	ttc agg ttc	aac cgg gca	gcg ctc atc	aac gtg ggc ttc		487
Val Asp His	Phe Arg Phe	Asn Arg Ala	Ala Leu Ile	Asn Val Gly	Phe	
	135		140		145	

ctg gag agc agc aac agc acg gac tac att gcc atg cac gac gtt gac Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp	150	155	160	165	535
ctg ctc cct ctc aac gag gag ctg gac tat ggc ttt cct gag gct ggg Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly	170	175	180		583
ccc ttc cac gtg gcc tcc ccg gag ctc cac cct ctc tac cac tac aag Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys	185	190	195		631
acc tat gtc ggc ggc atc ctg ctc tcc aag cag cac tac cgg ctg Thr Tyr Val Gly Gly Ile Leu Leu Ser Lys Gln His Tyr Arg Leu	200	205	210		679
tgc aat ggg atg tcc aac cgc ttc tgg ggc tgg ggc cgc gag gac gac Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp	215	220	225		727
gag ttc tac cgg cgc att aag gga gct ggg ctc cag ctt ttc cgc ccc Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro	230	235	240	245	775
tgc gga atc aca act ggg tac aag aca ttt cgc cac ctg cac gac cca Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro	250	255	260		823
gcc tgg cgg aag agg gac cag aag cgc atc gca gct caa aaa cag gag Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu	265	270	275		871
cag ttc aag gtg gac agg gag gga ggc ctg aac act gtg aag tac cat Gln Phe Lys Val Asp Arg Glu Gly Leu Asn Thr Val Lys Tyr His	280	285	290		919
gtg gct tcc cgc act gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val	295	300	305		967
ctc aac atc atg ttg gac tgt gac aag acc gcc aca ccc tgg tgc aca Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr	310	315	320	325	1015
ttc agc tga gctggatgga cagtgaggaa gcctgtacct acaggccata Phe Ser					1064
ttgctcaggc tcaggacaag gcctcaggc gtggggccag ctctgacagg atgtggagtg					1124
gccaggacca agacagcaag ctacgcaatt gcagccaccc ggccgccaag gcaggcttgg					1184
gctggggccag gacacgtggg gtgcctggga cgctgcttgc catgcacagt gatcagagag					1244
aggctgggt gtgtcctgtc cgggacccccc cctgccttcc tgctcacct actctgacct					1304
ccttcacgtg cccaggcctg tggtagtgg ggagggctga acaggacaac ctctcatcac					1364

ccccactttt gttccttcct gctgggctgc ctcgtgcaga gacacagtgt aggggccatg	1424
cagctggcgt aggtggcagt tgggcctggt gagggtagg acttcagaaa ccagagcaca	1484
agccccacag agggggaaca gccagcaccc ctctagctgg ttgttgccat gccggaatgt	1544
gggcctagtg ttgccagatc ttctgatttt tcgaaagaaa ctagaatgct ggattctaa	1604
gtgatatctt ctgattttt aaatgatagc acctaaatga aactttcaaa aagtaaaaaaa	1664
aaaaa	1669

<210> 6.
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
1 5 10 15

Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe
20 25 30

His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
35 40 45

Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
50 55 60

Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
65 70 75 80

Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
85 90 95

Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
100 105 110

Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
115 120 125

Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
130 135 140

Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
145 150 155 160

Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
165 170 175

Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
180 185 190

Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
 195 200 205
 Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
 210 215 220
 Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
 225 230 235 240
 Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
 245 250 255
 His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
 260 265 270
 Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
 275 280 285
 Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
 290 295 300
 Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
 305 310 315 320
 Thr Pro Trp Cys Thr Phe Ser
 325

<210> 7
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 5' primer for PCR (K3)

 <400> 7
 cccaaagcttg ccgaggggga gccccga

26

<210> 8
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 8
 gctcttagact gtcaggagag agttcgatt

29

<210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 9
atggctgtgc gctctcgccg cccgt

25

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 10
cgtccccgct gccgttgtgg ctact

25

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 11
atagccaca acggcagcgg ggacg

25

<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 12
tcaggagaga gttcgattgt acct

24

<210> 13
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR (K11)

<400> 13
ggaattccgg ccagggccgcc aaaaaggc

28

<210> 14
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR (K11)

<400> 14
cgggatcctc aggtgctgtt gccctgctcc

30

<210> 15
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthesised substance for assay

<400> 15

Val Leu Pro Gln Glu Glu Glu Gly Ser Gly Gly Gln Leu Val Thr
1 5 10 15

<210> 16
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K3 exon 1)

<400> 16
cgacagccca gcgagcgtcc

20

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 1)

<400> 17
ggagactggc aggctggaaa gc

22

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 1)

<400> 18

agggggagcc cgaggaggag

20

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 1)

<400> 19

ctcctccctcg ggctccccct

20

<210> 20

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (K3 exon 2)

<400> 20

gagacatagt aattgttgcc tttcttt

27

<210> 21

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and
sequencing (K3 exon 2)

<400> 21

gtgaacattt tcatcacagc tccat

25

<210> 22

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (K3 exon 3)

<400> 22

tagatgctt agtttatcgc tggttt

26

<210> 23
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 3)

<400> 23
ttaaaaaagg caaaatgtgt tgcctg

26

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 24
tctatactca gcagctgaga acca

24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 25
tggttctcag ctgctgagta taga

24

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 26
gaaatgggag ggcacaatga aaag

24

<210> 27
<211> 24
<212> DNA

<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 27
ctttcattg tgccctccca ttcc

24

<210> 28
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 28
tagccagttt gacccaaagg taac

24

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 29
gttacctttt ggtcatactg gcta

24

<210> 30
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 30
aggccattca gaagccaaga agtaggatg g

31

<210> 31
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K3 exon 3)

<400> 31	
ccactcctac ttcttggctt ctgaatggcc t	31
<210> 32	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 1)	
<400> 32	
tcggagactc ctctggctgc t	21
<210> 33	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Descriprion of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 1)	
<400> 33	
tagagcgggc gcagccgatc a	21
<210> 34	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 2)	
<400> 34	
tttgataagc ttgtgccatc tcctc	25
<210> 35	
<211> 25	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 2)	
<400> 35	
agtatcgtt gggatagctt atcat	25

<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 3)

<400> 36
agctcatcac agatcccttc cttt

24

<210> 37
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 1)

<400> 37
actctgccac ccccagacct ag

22

<210> 38
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 4)

<400> 38
ttgctgatgg cctgtttctc tgat

24

<210> 39
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 4)

<400> 39
gtgtggccat gccacggccc a

21

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K11 exon 4)

<400> 40
tatgtcactg aggccctcacg tct

23

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K11 exon 4)

<400> 41
agacgtgagg cctcagtgac ata

23

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer for sequencing
(K11 exon 4)

<400> 42
atgcatttcc aagccttcca cccca

24

<210> 43
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer for sequencing
(K11 exon 4)

<400> 43
tgggtgaaag gcttgaaat gcat

24

<210> 44
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and
sequencing (beta4Gal-T7 exon 1)

<400> 44

tgcgagcgcc tgccccatgc	20
<210> 45	
<211> 22	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 1)	
<400> 45	
gatggcctcg ggttcccaga tt	22
<210> 46	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 2)	
<400> 46	
tcctgaccct gtcccgcgct t	21
<210> 47	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 2)	
<400> 47	
aggggtgccg aggggagagg	20
<210> 48	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 3)	
<400> 48	
ctgcccagcc ttgcccaccc t	21
<210> 49	
<211> 22	

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 3)

<400> 49
gctctgagca gagcaggctg tc

22

<210> 50
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 4)

<400> 50
agatgggccg agtgacgctg ct

22

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 4)

<400> 51
ctcagggcag ccaccgcagc t

21

<210> 52
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 5)

<400> 52
aagggcagcc tgaccccgac tt

22

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and

sequencing (beta4Gal-T7 exon 5)

<400> 53
atgaccacct atccgtcccc aat 23

<210> 54
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 6)

<400> 54
cagccctgag tccgtgctct tt 22

<210> 55
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 6)

<400> 55
tggcctgttag gtacaggctt cct 23

<210> 56
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for RT-PCR (K3)

<400> 56
cccagaaaaaa gtccttcatg atg 23

<210> 57
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for RT-PCR (K3)

<400> 57
aactcttcta atttgtcacc tttgatgtag 30

<210> 58

<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe for RT-PCR (K3)

<400> 58
atgagtggtt catgcgc 17

<210> 59
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for RT-PCR (K11)

<400> 59
gctgaactgg aacgcacgta 20

<210> 60
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for RT-PCR (K11)

<400> 60
cgggatggtg ctggaatac 19

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe for RT-PCR (K11)

<400> 61
agatccagga gttacagtgg 20

<210> 62
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 5' primer for RT-PCR
(beta4Gal-T7)

<400> 62

cggcgattt agggagct

18

<210> 63
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: 3' primer for RT-PCR
(beta4Gal-T7)

<400> 63
tacccagttg tgattccccga g

21

<210> 64
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Probe for RT-PCR
(beta4Gal-T7)

<400> 64
ctccagcttt tccg

14

<210> 65
<211> 2652
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (1)..(2652)

<400> 65
atg gcc gtg cgc tcc cgc cgc cca tgg gtg agc gtg gca ttg ggg ttg
Met Ala Val Arg Ser Arg Arg Pro Trp Val Ser Val Ala Leu Gly Leu
1 5 10 15

48

gtc ctg ggc ttc acc gcc gcg tcc tgg ctc atc gcc ccc cgg gtg gcc
Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala
20 25 30

96

gag ctg agc gag aag agg cga cgc ggc tcc agt ctt tgc tcc tac tac
Glu Leu Ser Glu Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr
35 40 45

144

ggc cgc tcg gct acc ggg ccc cgc gcg gac gcg cag cag ctg ctc ccc
Gly Arg Ser Ala Thr Gly Pro Arg Ala Asp Ala Gln Gln Leu Leu Pro
50 55 60

192

caa ccc cag tcc cg ^g ccg cgg cta gag cag tcg ccg ccc cct gcc agc Gln Pro Gln Ser Arg Pro Arg Leu Glu Gln Ser Pro Pro Pro Ala Ser 65 70 75 80	240
cac gag ctc ccc ggt cct cag cag ccg gag gc ^g gc ^g ccc gga ggt ccc His Glu Leu Pro Gly Pro Gln Gln Pro Glu Ala Ala Pro Gly Gly Pro 85 90 95	288
agt ttt cgg agc agc ccc tgg cag cag ccg gct ctg ttg ccg cag agg Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Ala Leu Leu Pro Gln Arg 100 105 110	336
agg cga gga cac acg ccc gaa ggt gc ^g ac ^g gc ^g ctt ccc ggc gct ccg Arg Arg Gly His Thr Pro Glu Gly Ala Thr Ala Leu Pro Gly Ala Pro 115 120 125	384
gct gcc aaa ggg gaa cca gag gag gag gat ggg ggc gc ^g gct gac cct Ala Ala Lys Gly Glu Pro Glu Glu Asp Gly Gly Ala Ala Asp Pro 130 135 140	432
cgg aag ggt ggc cg ^g ccg ggg agc agc cac aac gg ^c agc ggg gac ggg Arg Lys Gly Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly 145 150 155 160	480
ggt gcc gct gtc ccg acc tcc gga ccc ggg gac ttc ctg tac gtg ggt Gly Ala Ala Val Pro Thr Ser Gly Pro Asp Phe Leu Tyr Val Gly 165 170 175	528
gtg atg acc gca cag aag tac ctg gg ^c agt cg ^c gc ^g ctg gcc gc ^g cag Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln 180 185 190	576
cgg acc tgg gc ^g cgc ttc atc cct gg ^c cgc gtg gag ttc ttt tcc agt Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser 195 200 205	624
cag caa tct ccc agt gct gc ^g ctt gg ^c cag ccc ccg cca cct ttg cct Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Leu Pro 210 215 220	672
gtc atc gc ^g ctg cca ggg gtc gac gat tcc tac cct ccc cag aaa aag Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys 225 230 235 240	720
tcc ttc atg atg atc aag tac atg cac gac cac tat ctg gac aag tat Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr 245 250 255	768
gag tgg ttc atg cgc gc ^c gac gac gat gtc tac atc aaa ggt gat aag Glu Trp Phe Met Arg Ala Asp Asp Val Tyr Ile Lys Gly Asp Lys 260 265 270	816
tta gaa gaa ttt cta aga tcc cta aat agc agc aag cct ctc tac ctg Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu 275 280 285	864

gga cag acg ggc ctg ggc aat act gaa gaa ctt gga aag ctg ggg ctg Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu	912
290 295 300	
gag ccc ggg gag aac ttc tgc atg gga gga cct ggc atg atc ttc agc Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser	960
305 310 315 320	
aga gag gtt ctc agg cgg atg gtg cct cat atc ggc gaa tgc ctc cga Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg	1008
325 330 335	
gag atg tac acc aca cac gaa gac gta gaa gta gga agg tgt gtt cgc Glu Met Tyr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg	1056
340 345 350	
cgt ttc ggc ggg acg cag tgt gtc tgg tct tat gag atg cag cag ctg Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu	1104
355 360 365	
ttc cat gaa aac tac gaa cac aat cgc aag ggt tac atc caa gac ctc Phe His Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu	1152
370 375 380	
cac aac agc aaa atc cac gca gcc atc acg ctc cat ccg aac aaa agg His Asn Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg	1200
385 390 395 400	
ccc gcg tac cag tac aga ctt cat aac tac atg ctc agc cgc aag atc Pro Ala Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile	1248
405 410 415	
tcc gag ctc cgc tac cgc acc atc cag ctc cac ccg gag agc gct ctc Ser Glu Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu	1296
420 425 430	
atg agc aag ctc agc aac agt gaa gtg agc aaa gag gac caa cag ctg Met Ser Lys Leu Ser Asn Ser Glu Val Ser Lys Glu Asp Gln Gln Leu	1344
435 440 445	
gga agg acg ccg tcc ttc aac cac ttc cag cct ccg gag aga aat gaa Gly Arg Thr Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu	1392
450 455 460	
gtc atg gag tgg gag ttc ctg acg ggg aag ctg ctt tac tca gct gca Val Met Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala	1440
465 470 475 480	
gag aac cag cct cgt cga cag agc atc aac agc atc cta agg tca gct Glu Asn Gln Pro Pro Arg Gln Ser Ile Asn Ser Ile Leu Arg Ser Ala	1488
485 490 495	
ctg gat gac act gtc ctg cag gtg atg gag atc aac gag aat gcc Leu Asp Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala	1536
500 505 510	

aag agt agg ggc cga ctc atc gac ttc aag gaa att cag tat ggc tac Lys Ser Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr 515 520 525	1584
cgc agg gtt gat ccc atg cac ggg gtt gag tac ata ttg gac ctg cta Arg Arg Val Asp Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu 530 535 540	1632
ctc ctg tac aaa agg cac aaa gga agg aaa ctg act gtg cct gtg agg Leu Leu Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg 545 550 555 560	1680
cgc cat gcc tat ctt cag cag cca ttt agc aag cct ttc ttc aga gag Arg His Ala Tyr Leu Gln Gln Pro Phe Ser Lys Pro Phe Phe Arg Glu 565 570 575	1728
gtg gaa gaa ctc gac gtc aac cgt ctg gtg gag agt atc aac agc ggt Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly 580 585 590	1776
aca cag tca ttc tcc gtt ata tcc aat tct cta aaa att ctc tct tct Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser 595 600 605	1824
ctt caa gag gcc aaa gac ata gga ggg cac aat gaa aag aaa gta cac Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His 610 615 620	1872
att ctc gtt cca ctc gtt gga agg tac gac att ttc ttg aga ttc atg Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met 625 630 635 640	1920
gaa aat ttt gaa agt acg tgt ctt atc cca aagcaa aat gtc aag ctt Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu 645 650 655	1968
gtc atc atc ctt ttc agc agg gat gct ggc caa gag tcc atc aag cac Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His 660 665 670	2016
att gag ctg ata caa gaa tat cag agc agg tat ccc agt gca gaa atg Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met 675 680 685	2064
atg ctc att ccc atg aag gga gag ttt tcc aga ggt ctt ggt ctt gaa Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu 690 695 700	2112
atg gct tct tcc cag ttt gac aat gac aca ttg ctg cta ttt tgt gat Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp 705 710 715 720	2160
gtt gac ttg att ttc aga gga gac ttc ctc caa cgc tgt cga gac aat Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn 725 730 735	2208

aca gtt cag gga caa cag gta tat tac ccc atc atc ttt agc cag tat		2256	
Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr			
740	745	750	
gac cca aag gtc acc cat atg aga aat cct ccc aca gag ggt gac ttt		2304	
Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe			
755	760	765	
gta ttc tca aag gaa act ggg ttt tgg aga gac tat ggc tac gga atc		2352	
Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile			
770	775	780	
aca tgc att tac aaa agc gat cta ctg ggt gca ggt gga ttt gat acc		2400	
Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr			
785	790	795	800
tca ata caa ggc tgg gga ctg gaa gat gta gat ctc tat aat aaa gtc		2448	
Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val			
805	810	815	
atc cta tct ggc tta cg ^g ccc ttc aga agt caa gaa gtg gga gtg gtg		2496	
Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val			
820	825	830	
cat att ttc cat cct gtt cat tgt gat cct aac ttg gac cct aag cag		2544	
His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln			
835	840	845	
tat aag atg tgc tta gga tcc aaa gca agt act ttt gcc tca acc atg		2592	
Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met			
850	855	860	
caa ctg gct gaa ctc tgg tta gaa aaa cat ttg ggt gtc agg gat aat		2640	
Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn			
865	870	875	880
cga act ctc tcc		2652	
Arg Thr Leu Ser			

<210> 66
<211> 884
<212> PRT
<213> mouse

<400> 66			
Met Ala Val Arg Ser Arg Arg Pro Trp Val Ser Val Ala Leu Gly Leu			
1	5	10	15
Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala			
20	25	30	
Glu Leu Ser Glu Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr			
35	40	45	
Gly Arg Ser Ala Thr Gly Pro Arg Ala Asp Ala Gln Gln Leu Leu Pro			
50	55	60	

Gln Pro Gln Ser Arg Pro Arg Leu Glu Gln Ser Pro Pro Pro Ala Ser
 65 70 75 80
 His Glu Leu Pro Gly Pro Gln Gln Pro Glu Ala Ala Pro Gly Gly Pro
 85 90 95
 Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Ala Leu Leu Pro Gln Arg
 100 105 110
 Arg Arg Gly His Thr Pro Glu Gly Ala Thr Ala Leu Pro Gly Ala Pro
 115 120 125
 Ala Ala Lys Gly Glu Pro Glu Glu Asp Gly Gly Ala Ala Asp Pro
 130 135 140
 Arg Lys Gly Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
 145 150 155 160
 Gly Ala Ala Val Pro Thr Ser Gly Pro Gly Asp Phe Leu Tyr Val Gly
 165 170 175
 Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
 180 185 190
 Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
 195 200 205
 Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Pro Leu Pro
 210 215 220
 Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys
 225 230 235 240
 Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr
 245 250 255
 Glu Trp Phe Met Arg Ala Asp Asp Val Tyr Ile Lys Gly Asp Lys
 260 265 270
 Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu
 275 280 285
 Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu
 290 295 300
 Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser
 305 310 315 320
 Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg
 325 330 335
 Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg
 340 345 350
 Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu
 355 360 365

Phe His Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu
 370 375 380

 His Asn Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg
 385 390 395 400

 Pro Ala Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile
 405 410 415

 Ser Glu Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu
 420 425 430

 Met Ser Lys Leu Ser Asn Ser Glu Val Ser Lys Glu Asp Gln Gln Leu
 435 440 445

 Gly Arg Thr Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu
 450 455 460

 Val Met Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala
 465 470 475 480

 Glu Asn Gln Pro Pro Arg Gln Ser Ile Asn Ser Ile Leu Arg Ser Ala
 485 490 495

 Leu Asp Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala
 500 505 510

 Lys Ser Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr
 515 520 525

 Arg Arg Val Asp Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu
 530 535 540

 Leu Leu Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg
 545 550 555 560

 Arg His Ala Tyr Leu Gln Gln Pro Phe Ser Lys Pro Phe Phe Arg Glu
 565 570 575

 Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly
 580 585 590

 Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser
 595 600 605

 Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His
 610 615 620

 Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met
 625 630 635 640

 Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu
 645 650 655

 Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His
 660 665 670

Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met
 675 680 685
 Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu
 690 695 700
 Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp
 705 710 715 720
 Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn
 725 730 735
 Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr
 740 745 750
 Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe
 755 760 765
 Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile
 770 775 780
 Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr
 785 790 795 800
 Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val
 805 810 815
 Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val
 820 825 830
 His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln
 835 840 845
 Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met
 850 855 860
 Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn
 865 870 875 880
 Arg Thr Leu Ser

<210> 67
 <211> 2490
 <212> DNA
 <213> mouse

<220>
 <221> CDS
 <222> (1)..(2325)

<400> 67

atg	cg	gc	tc	ct	ct	tcc	gt	ct	cg	cc	gc	gg	cc	gt		48	
Met	Arg	Ala	Ser	Leu	Leu	Leu	Ser	Val	Leu	Arg	Pro	Ala	Gly	Pro	Val		
1				5				10						15			
gcc	gt	gg	atc	tct	ct	gg	t	tc	acc	ct	agc	ct	tc	agc	gt		96
Ala	Val	Gly	Ile	Ser	Leu	Gly	Phe	Thr	Leu	Ser	Leu	Leu	Ser	Val	Thr		
20					25									30			
tgg	gt	ga	ga	cct	tg	gg	cc	gg	cc	cc	ca	cc	gg	ga	ac	tct	144
Trp	Val	Glu	Glu	Pro	Cys	Gly	Pro	Gly	Pro	Pro	Gln	Pro	Gly	Asp	Ser		
35							40					45					
gag	ct	cg	cc	cg	gg	aa	ac	ac	g	cg	cg	cg	cc	aa	tc		192
Glu	Leu	Pro	Pro	Arg	Gly	Asn	Thr	Asn	Ala	Ala	Arg	Arg	Arg	Pro	Asn	Ser	
50						55					60						
gt	ca	cc	gg	tcc	ga	cg	ga	gg	cc	gg	cc	gca	gg	ac		240	
Val	Gln	Pro	Gly	Ser	Glu	Arg	Glu	Arg	Pro	Gly	Ala	Gly	Ala	Gly	Thr		
65					70				75			80					
ggt	ga	ag	tgg	ga	cct	cgt	gt	t	ccc	ta	cat	cc	g	ca	cc		288
Gly	Glu	Ser	Trp	Glu	Pro	Arg	Val	Leu	Pro	Tyr	His	Pro	Ala	Gln	Pro		
85						90					95						
gg	ca	gc	ac	aa	aa	gg	cc	gt	ag	act	cg	tt	at	ac	ac	ga	336
Gly	Gln	Ala	Thr	Lys	Lys	Ala	Val	Arg	Thr	Arg	Tyr	Ile	Ser	Thr	Glu		
100						105					110						
ct	gg	atc	agg	cag	aa	ctt	ct	gt	gca	gt	ct	ac	tca	ca	gg		384
Leu	Gly	Ile	Arg	Gln	Lys	Leu	Leu	Val	Ala	Val	Leu	Thr	Ser	Gln	Ala		
115						120					125						
ac	tt	c	ca	ct	gg	gt	g	ct	gt	gt	aa	ca	ct	gg	ca	cc	432
Thr	Leu	Pro	Thr	Leu	Gly	Val	Ala	Val	Asn	Arg	Thr	Leu	Gly	His	Arg		
130						135					140						
ct	ga	ca	gt	gt	t	tc	ct	ac	gg	ag	gg	cc	ca	cc		480	
Leu	Glu	His	Val	Val	Phe	Leu	Thr	Gly	Ala	Arg	Gly	Arg	Arg	Thr	Pro		
145						150				155			160				
tca	gg	at	gc	gt	gt	gca	ct	gg	ga	ga	gg	cc	atc	gg	ca		528
Ser	Gly	Met	Ala	Val	Val	Ala	Leu	Gly	Glu	Glu	Arg	Pro	Ile	Gly	His		
165							170					175					
ct	ca	ct	gc	ct	cg	ca	ct	gt	ga	ca	ca	cc	gg	at	gt	tt	576
Leu	His	Leu	Ala	Leu	Arg	His	Leu	Leu	Glu	Gln	His	Gly	Asp	Asp	Phe		
180							185				190						
gac	tgg	ttt	t	tc	ta	gt	c	ct	gt	at	ac	tt	gg	ca	cc		624
Asp	Trp	Phe	Phe	Leu	Val	Pro	Asp	Ala	Thr	Tyr	Thr	Glu	Ala	His	Gly		
195							200				205						
ct	ga	cg	ct	gg	ca	ct	gt	ct	gt	ca	ac	ca	cc	at	ct		672
Leu	Asp	Arg	Leu	Ala	Gly	His	Leu	Ser	Leu	Ala	Ser	Ala	Thr	His	Leu		
210							215				220						

tat ctt ggc cg ^c ccg cag gac ttc atc ggt gga gat act acc cca ggc Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly 225 230 235 240	720
cgc tac tgc cac ggg ggc ttt gga gtc ttg ctc tct cgc aca ctg cta Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu 245 250 255	768
cag caa ctg cgc ccc cac ctg gaa agc tgc cgc aac gac atc gtc agt Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser 260 265 270	816
gct cgc ccg gat gag tgg ttg ggc cgc tgc atc ctt gat gcc aca ggc Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly 275 280 285	864
gtg ggc tgt act ggt gac cac gag gga atg cac tac aac tac ctg gaa Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu 290 295 300	912
ctg agc ccc ggg gag cct gta cag gag ggg gac cct cgt ttc cgc agc Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser 305 310 315 320	960
gcc ttg aca gcc cat ccc gtg cgt gac cct gtg cac atg tac cag ctg Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu 325 330 335	1008
cac aaa gct ttt gcc cgc gct gag ctg gac cgc acg tac cag gag att His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile 340 345 350	1056
caa gaa ttg cag tgg gag atc cag aat acc agc cga ctg gct gct gat Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp 355 360 365	1104
ggg gag aga gcc tct gcc tgg cca gtg ggc atc cca gca ccg tct cgc Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg 370 375 380	1152
cct gcc tca cgc ttt gag gtt ctg cgc tgg gac tac ttc aca gaa caa Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln 385 390 395 400	1200
tac gcg ttc tcc tgc gcc gat ggc tct ccc cgc tgc ccg ttg cgt ggg Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly 405 410 415	1248
gcc gac cag gct gat gtg gct gac gtc ctg ggg aca gcc tta gag gag Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu 420 425 430	1296
ctc aac cgc cgt tac cag cca gcg ctg cag ctc cag aag caa cag ctg Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Gln Lys Gln Gln Leu 435 440 445	1344

gtg aac ggc tac cgg cgt ttt gat cca gcc cga ggc atg gag tac aca Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr 450 455 460	1392
cta gac ctg cag ctg gaa gcg ctg aca ccc cag ggt ggc cgc tgg ccc Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro 465 470 475 480	1440
ctc acc cgc agg gtg cag ctc ctt cgg ccc ttg agc cga gtg gag atc Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile 485 490 495	1488
ttg cct gta ccc tat gtc acc gag gct tct cgg ctc act gtg cta ctg Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu 500 505 510	1536
ccg ctg gct gca gcg gaa cga gac ctg gct tct ggc ttc tta gaa gcc Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala 515 520 525	1584
ttt gcc act gca gcc ctg gaa cct ggt gat gca gca gcc ttg acc ctg Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Leu Thr Leu 530 535 540	1632
ctg ctg ctg tat gag cca cgc cag gcc cag cgg gca gcc cac tca gac Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp 545 550 555 560	1680
gtc ttc gca cct gtc aag gcc cac gtg gca gag cta gag cgg cgt ttc Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe 565 570 575	1728
cct ggt gcc cgg gtg ccc tgg ctc agt gtg cag aca gca gcg ccc tct Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser 580 585 590	1776
cca ctg cgt ctc atg gat ctg ctg tcc aag aag cac cca cta gac act Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr 595 600 605	1824
ctg ttc ctg ctg gcc ggg cca gac acg gta ctc aca cct gat ttc ctg Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu 610 615 620	1872
aac cgc tgc cgc atg cat gcc atc tct ggc tgg cag gcc ttc ttc ccc Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro 625 630 635 640	1920
atg cac ttc cag gcc ttc cac cct gct gtg gct cct cct cag ggc cct Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro 645 650 655	1968
ggg cca cca gag ctg ggc cgt gac acc ggt cac ttt gat cgc cag gct Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala 660 665 670	2016

gcc agt gag gca tgc ttc tac aac tcc gac tat gtg gcg gcc cgt ggc		2064	
Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly			
675	680	685	
cgg ctg gtg gcg gcc tcg gag cag gag gag ctg ctg gag agc ctg		2112	
Arg Leu Val Ala Ala Ser Glu Gln Glu Glu Leu Leu Glu Ser Leu			
690	695	700	
gat gtg tac gag ttg ttt ctg cgc ttc tcc aac ttg cac gtg ctg aga		2160	
Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg			
705	710	715	720
gca gta gag cca gcc ttg ctg cag cgc tac cgg gcc cag ccg tgc agt		2208	
Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser			
725	730	735	
gca cgg ctc agt gaa gac ctt tac cac cgc tgt cgc cag agc gta ctt		2256	
Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu			
740	745	750	
gag ggc ctt ggc tcc cgc acc cag ctt gcc atg ctg ctc ttt gag cag		2304	
Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln			
755	760	765	
gaa cag ggg aac agc acc taa gcccctgcac ctgtccctgc tcttccccag		2355	
Glu Gln Gly Asn Ser Thr			
770			
gaacctggag ccacgtgcca gcctcgctgg acagggctgg ctgtagccctc agtccctagg		2415	
gcagccccact ggtcccttgt ctcttgcttt gttggaccctt tgggctcagg acaagccctg		2475	
agacagatgc cctag		2490	
<210> 68			
<211> 774			
<212> PRT			
<213> mouse			
<400> 68			
Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val			
1	5	10	15
Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr			
20	25	30	
Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser			
35	40	45	
Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser			
50	55	60	
Val Gln Pro Gly Ser Glu Arg Glu Arg Pro Gly Ala Gly Ala Gly Thr			
65	70	75	80

Gly Glu Ser Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro
 85 90 95

 Gly Gln Ala Thr Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu
 100 105 110

 Leu Gly Ile Arg Gln Lys Leu Leu Val Ala Val Leu Thr Ser Gln Ala
 115 120 125

 Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg
 130 135 140

 Leu Glu His Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Thr Pro
 145 150 155 160

 Ser Gly Met Ala Val Val Ala Leu Gly Glu Arg Pro Ile Gly His
 165 170 175

 Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe
 180 185 190

 Asp Trp Phe Phe Leu Val Pro Asp Ala Thr Tyr Thr Glu Ala His Gly
 195 200 205

 Leu Asp Arg Leu Ala Gly His Leu Ser Leu Ala Ser Ala Thr His Leu
 210 215 220

 Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly
 225 230 235 240

 Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu
 245 250 255

 Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser
 260 265 270

 Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly
 275 280 285

 Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu
 290 295 300

 Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser
 305 310 315 320

 Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
 325 330 335

 His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile
 340 345 350

 Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp
 355 360 365

 Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
 370 375 380

Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
385 390 395 400

Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
405 410 415

Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
420 425 430

Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Gln Lys Gln Gln Leu
435 440 445

Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
450 455 460

Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro
465 470 475 480

Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
485 490 495

Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
500 505 510

Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala
515 520 525

Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Leu Thr Leu
530 535 540

Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp
545 550 555 560

Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe
565 570 575

Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser
580 585 590

Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr
595 600 605

Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu
610 615 620

Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro
625 630 635 640

Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro
645 650 655

Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala
660 665 670

Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly
675 680 685

Arg Leu Val Ala Ala Ser Glu Glu Glu Glu Leu Leu Glu Ser Leu
690 695 700

Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg
705 710 715 720

Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser
725 730 735

Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu
740 745 750

Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln
755 760 765

Glu Gln Gly Asn Ser Thr
770

<210> 69
<211> 984
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (1)...(984)

<400> 69					
atg ttg ccc tcc cgg agg aaa gcg gcg cag ctg ccc tgg gag gat ggc					48
Met Leu Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly					
1 5 10 15					
agg gcc agg ttg ctt cct gga ggc ctc cgc cgg aaa tgc tcc atc ttc					96
Arg Ala Arg Leu Leu Pro Gly Gly Leu Arg Arg Lys Cys Ser Ile Phe					
20 25 30					
cac ctc ttc att gcc ttt ctc ctg ttg gtc ttc tcc ctg ctc tgg					144
His Leu Phe Ile Ala Phe Leu Leu Val Phe Phe Ser Leu Leu Trp					
35 40 45					
ctg cag ctc agc tgt tct gga gat atg gcc cag gtg acc agg gga caa					192
Leu Gln Leu Ser Cys Ser Gly Asp Met Ala Gln Val Thr Arg Gly Gln					
50 55 60					
ggg caa gag acc tcg ggt cca ccc cgg gct tgc cct cca gag ccg ccc					240
Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro					
65 70 75 80					
cct gag cac tgg gaa gaa gat gag tcc tgg ggg ccc cac cgc ttg gca					288
Pro Glu His Trp Glu Glu Asp Glu Ser Trp Gly Pro His Arg Leu Ala					
85 90 95					
gtg ctg gtg ccc ttt cgt gag cgc ttt gag gag ctg ctg gtc ttt gtg					336
Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val					
100 105 110					

ccc cac atg cac cgc ttc cta agc agg aag agg atc cag cac cac atc Pro His Met His Arg Phe Leu Ser Arg Lys Arg Ile Gln His His Ile	384
115 120 125	
tat gtg ctc aac cag gtg gac cat ttc agg ttc aat cgg gca gca ctc Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu	432
130 135 140	
atc aat gtg ggc ttc ctg gag agc agc aac agc aca gac tac atc gcc Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala	480
145 150 155 160	
atg cac gat gtg gac ctg ctc cct ctc aat gag gag ctg gac tat ggc Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly	528
165 170 175	
ttc ccg gag gct ggg ccc ttc cat gtg gcc tcc cca gag ctc cac cct Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro	576
180 185 190	
ctc tac cac tac aag acc tat gtg ggc att ctg ctg ctg tcc aaa Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys	624
195 200 205	
cag cac tac cag ctg tgc aac gga atg tcc aac cgc ttt tgg ggc tgg Gln His Tyr Gln Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp	672
210 215 220	
ggc cga gag gat gat gaa ttc tac cgg cgc atc aaa gga gct ggc ctc Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu	720
225 230 235 240	
cag ctt ttc cgc ccc tcg gga atc aca act ggg tac cag aca ttt cgc Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Gln Thr Phe Arg	768
245 250 255	
cac ttg cat gac cct gcc tgg cgg aag agg gac caa aaa cgc att gcg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala	816
260 265 270	
gct caa aaa cag gaa cag ttc aag gtg gac cgg gag gga ggc ctg aac Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn	864
275 280 285	
act gtg aag tac cgg gtg gat tcc cgc acg gca ctg tct ata gga ggg Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly	912
290 295 300	
gcc ccg tgc act gtc ctc aat gtc atg ctg gac tgc gat aaa aca gcc Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala	960
305 310 315 320	
acc cca tgg tgc ata ttt ggc tga Thr Pro Trp Cys Ile Phe Gly	984
325	

<210> 70
 <211> 327
 <212> PRT
 <213> mouse

<400> 70
 Met Leu Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
 1 5 10 15

Arg Ala Arg Leu Leu Pro Gly Gly Leu Arg Arg Lys Cys Ser Ile Phe
 20 25 30

His Leu Phe Ile Ala Phe Leu Leu Val Phe Phe Ser Leu Leu Trp
 35 40 45

Leu Gln Leu Ser Cys Ser Gly Asp Met Ala Gln Val Thr Arg Gly Gln
 50 55 60

Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
 65 70 75 80

Pro Glu His Trp Glu Glu Asp Glu Ser Trp Gly Pro His Arg Leu Ala
 85 90 95

Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
 100 105 110

Pro His Met His Arg Phe Leu Ser Arg Lys Arg Ile Gln His His Ile
 115 120 125

Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
 130 135 140

Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
 145 150 155 160

Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
 165 170 175

Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
 180 185 190

Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
 195 200 205

Gln His Tyr Gln Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
 210 215 220

Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
 225 230 235 240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Gln Thr Phe Arg
 245 250 255

His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
 260 265 270

Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
275 280 285

Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly
290 295 300

Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala
305 310 315 320

Thr Pro Trp Cys Ile Phe Gly
325